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searching Seq2 library
Comparison of:
(A) Seq1        >Seq1   (540 nucleotides)        SEQ ID NO: 1           - 540 nt
(B) Seq2        >Seq2   (540 nucleotides)        SEQ ID NO: 3           - 540 nt
using matrix file DNA

    99.3% identity in 540 nt overlap; init: 2132, opt: 2132

                   10        20        30        40        50        60
Seq1   ATGCCGATCGAGTACAAGCCTGAAATCCAGCACTCCGATTTCAAGGACCTGACCAACCTG
       X::::::: :  ::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2   ATGCCGATCAAGTACAAGCCTGAAATCCAGCACTCCGATTTCAAGGACCTGACCAACCTG
                   10        20        30        40        50        60

                   70        80        90       100       110       120
Seq1   ATCCACTTCCAGAGCATGGAAGGCAAGATCTGGCTTGGCGAACAGCGCATGCTGTTGCTG
       :::::::::::::::::::::::::::::::::::::::::::::::: :::::::::::::
Seq2   ATCCACTTCCAGAGCATGGAAGGCAAGATCTGGCTTGGCGAACAACGCATGCTGTTGCTG
                   70        80        90       100       110       120

                  130       140       150       160       170       180
Seq1   CAGTCTTCAGCGATGGCCAGCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGC
       ::::: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2   CAGTTTTCAGCGATGGCCAGCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGC
                  130       140       150       160       170       180

                  190       200       210       220       230       240
Seq1   GCCAAGGGCTTGTTCCTGCGCCATGGTTACCAGTCCGGCCTGAAGGATGCCGAACTGGCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2   GCCAAGGGCTTGTTCCTGCGCCATGGTTACCAGTCCGGCCTGAAGGATGCCGAACTGGCC
                  190       200       210       220       230       240

                  250       260       270       280       290       300
Seq1   AGGAAGCTGAGACCGAATGCCAGCGAAGTCGGCATGTTCCTCGCTGGGCCGCAGATGCAT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2   AGGAAGCTGAGACCGAATGCCAGCGAAGTCGGCATGTTCCTCGCTGGGCCGCAGATGCAT
                  250       260       270       280       290       300

                  310       320       330       340       350       360
Seq1   TCACTCAAGGGTCTGGTCAAGGTCCGCCCCACCGAGCTCGATATCGACAAGGAATACGGG
       :::::::::::::::::::::::::::::::::::: :::::::::::::::::::::::::
Seq2   TCACTCAAGGGTCTGGTCAAGGTCCGCCCCACCGGGCTCGATATCGACAAGGAATACGGG
                  310       320       330       340       350       360

                  370       380       390       400       410       420
Seq1   CGCTTCTATGCCGAGATGGAGTGGATCGACTGGTTCGAGGTGGAAATCTGCCAGACCGAC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2   CGCTTCTATGCCGAGATGGAGTGGATCGACTGGTTCGAGGTGGAAATCTGCCAGACCGAC
                  370       380       390       400       410       420

                  430       440       450       460       470       480
Seq1   CTGGGGCAGATGCAAGACCCGGTGTGCTGGACTGTGCTCGGCTACGCCTGCGCCTATTCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2   CTGGGGCAGATGCAAGACCCGGTGTGCTGGACTGTGCTCGGCTACGCCTGCGCCTATTCC
                  430       440       450       460       470       480

                  490       500       510       520       530       540
Seq1   TCGGCGTTCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGCGGC
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::X
Seq2   TCGGCGTTCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGCGGC
                  490       500       510       520       530       540

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  54.5% identity in 55 nt overlap; init:    40, opt:    45


             490         500         510         520         530
Seq1    GGCGTTCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGC
        :::     : :   X:::::::::X  ::    :       : ::    :::: :    :::
Seq2    GGCCAGCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGCGCCAAGGGC
            140         150         160         170         180
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  52.7% identity in 110 nt overlap; init:    40, opt:    49


             90          100         110         120         130
Seq1    AGGCAAGATCTGGCTTGGCGAACAGCGC-ATGCTGTTGCTGCAGTCTTCAGCGATGGCCA
        :  :::::::  :  ::    ::   :  ::  :  ::     :::    ::::    :  :    :     :::
Seq2    ATGCAAGACCCGGTGTGCTGGACTGTGCTCGGCTACGCCTGC--GCCTATTCCTCGGCGT
          430         440         450         460         470         480


        140         150         160         170         180
Seq1    GCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGCGCCAAGGGC
        :  :   X:::::::::X  ::    :        : :: :    :::: :    :::
Seq2    TCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGC
          490         500         510         520         530
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